

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Schmidt, Robert R.
Miller, Philip

(ii) TITLE OF INVENTION: NOVEL POLYPEPTIDES AND POLYNUCLEOTIDES
RELATING TO THE α - AND β -SUBUNITS OF GLUTAMATE
DEHYDROGENASES AND METHODS OF USE

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Saliwanchik & Saliwanchik
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(C) CITY: Gainesville
(D) STATE: Florida
(E) COUNTRY: USA
(F) ZIP: 32606-6669

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/070,844
(B) FILING DATE: 01-MAY-98

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/725,596
(B) FILING DATE: 03-OCT-96

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/541,033
- (B) FILING DATE: 06-OCT-95

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Lloyd, Jeff
- (B) REGISTRATION NUMBER: 35,589
- (C) REFERENCE/DOCKET NUMBER: UF-155CD3

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (352) 375-8100
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..1610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCTTTCTG CTCGCCCTCT CTCCGTCCCCG CC ATG CAG ACC GCC CTC GTC GCC
Met Gln Thr Ala Leu Val Ala
1 5

53

AAG CCT ATC GTG GCC GCC CCG CTG GCG GCA CGC CCG CGC TGC CTC GCG
Lys Pro Ile Val Ala Ala Pro Leu Ala Ala Arg Pro Arg Cys Leu Ala
10 15 20

101

CCG TGG CCG TGC GCG TGG GTC CGC TCC GCC AAG CGC GAT GTC CGC GCC	149		
Pro Trp Pro Cys Ala Trp Val Arg Ser Ala Lys Arg Asp Val Arg Ala			
25	30	35	
AAG GCC GTC TCG CTG GAG GAG CAG ATC TCC GCG ATG GAC GCC ACC ACC	197		
Lys Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr Thr			
40	45	50	55
GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG AAG CAG ATG GCC ACC AAG	245		
Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala Thr Lys			
60	65	70	
GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC AAG AAC CCC GAC GTG CGC	293		
Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp Val Arg			
75	80	85	
CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC CCG GAG CAG GAG TTC	341		
Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Glu Phe			
90	95	100	
ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC CTG CAG CCC GTG TTC GAG	389		
Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val Phe Glu			
105	110	115	
AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG CAG ATC GTT GAG CCT GAG	437		
Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu Pro Glu			
120	125	130	135
CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG GAC GAC GCC GGC AAC CTG	485		
Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly Asn Leu			
140	145	150	
CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC TCG TCC GCC ATC GGC CCC	533		
Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile Gly Pro			
155	160	165	
TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC GTG AAC CTG TCC ATC ATG	581		
Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile Met			
170	175	180	

AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG AAC AGC CTG ACC ACC CTG Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr Thr Leu 185 190 195	629
CCC ATG GGC GGC GGC AAG GGC GGC TCC GAC TTC GAC CCC AAG GGC AAG Pro Met Gly Gly Lys Gly Ser Asp Phe Asp Pro Lys Gly Lys 200 205 210 215	677
AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG TCC TTC ATG ACC GAG CTG Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr Glu Leu 220 225 230	725
CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG CCC GCC GGC GAC ATC GGC Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp Ile Gly 235 240 245	773
GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC GGC CAG TAC AAG CGC ATC Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys Arg Ile 250 255 260	821
ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG AAG GGC CAG GAG TAT GGC Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu Tyr Gly 265 270 275	869
GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC TAC GGC GCC GTG CTG TTT Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val Leu Phe 280 285 290 295	917
GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG AGC CTC AAG GGC AAG CGC Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly Lys Arg 300 305 310	965
TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC CAG TAC TGC GCG GAG CTG Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala Glu Leu 315 320 325	1013
CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG CTG TCC GAC TCC CAG GGC Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser Gln Gly 330 335 340	1061

TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC GAG CAG CTG CAG GCG GTG	1109		
Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln Ala Val			
345	350	355	
CAG GAC ATG AAG AAG AAC AAC AGC GCC CGC ATC TCC GAG TAC AAG	1157		
Gln Asp Met Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu Tyr Lys			
360	365	370	375
AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC CGC AAG CCT TGG GAG CTG	1205		
Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp Glu Leu			
380	385	390	
GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC GCC ACC CAG AAC GAG ATC	1253		
Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn Glu Ile			
395	400	405	
GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG CAC GGC TGC CAG TAC GTG	1301		
Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln Tyr Val			
410	415	420	
GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC GAG GCC ATC CAC AAG TAC	1349		
Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His Lys Tyr			
425	430	435	
AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC AAG GCG GCC AAC GCC GGC	1397		
Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn Ala Gly			
440	445	450	455
GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC CAG AAC CGC ATG AGC CTG	1445		
Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met Ser Leu			
460	465	470	
AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG CTG GAG CGC ATC ATG AAG	1493		
Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile Met Lys			
475	480	485	

GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC CGC AGA TAC AAT GTT GAC	1541	
Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn Val Asp		
490	495	500
CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC ACC AAG GTG GCT GAT GCC	1589	
Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala Asp Ala		
505	510	515
GTC AAG GCC CAG GGC GCT GTT TAAAGCTGCC AGGCCAAGC CACGGCTCAC	1640	
Val Lys Ala Gln Gly Ala Val		
520	525	
CGGCAATCCA ACCCAACCAA CTCAACGGCC AGGACCTTTT CGGAAGCGGC GCCTTTTCC	1700	
CAGCCAGGGC CCTCACCTGC CCTTCATAA CCCTGCTATT GCCGCCGTGC CCCTGCAATT	1760	
CCACCCCAAG AAGAACTAGC GGCACTTGAC TGCATCAGGA CGGCTATTTT TTTCGCGACG	1820	
CGCGCTCACC CCGAGAGCCT CTCTCCCCG AGCCCTAAGC GCTGACGTCC GCCCGACTTT	1880	
GCCTCGCACA TCGCTCGGTT TTGACCCCT CCAGTCTACC CACCTGTTG TGAAGCCTAC	1940	
CAGCTCAATT GCCTTTAGT GTATGTGCGC CCCCTCCTGC CCCCGAATT TCCTGCCATG	2000	
AGACGTGCGG TTCCTAGCCT GGTGACCCCA AGTAGCAGTT AGTGTGCGTG CCTTGCCCTG	2060	
CGCTGCCCGG GATGCGATAC TGTGACCTGA GAGTGCTTGT GTAAACACGA CGAGTCAAAA	2120	
AAAAAAAAAA AAAAAAAAAA	2140	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gln Thr Ala Leu Val Ala Lys Pro Ile Val Ala Ala Pro Leu Ala
1 5 10 15

Ala Arg Pro Arg Cys Leu Ala Pro Trp Pro Cys Ala Trp Val Arg Ser
20 25 30

Ala Lys Arg Asp Val Arg Ala Lys Ala Val Ser Leu Glu Glu Gln Ile
35 40 45

Ser Ala Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala
50 55 60

Val Lys Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly
65 70 75 80

Ile Lys Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys
85 90 95

Asp Pro Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val Ala Val
100 105 110

Ser Leu Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe
115 120 125

Lys Gln Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp
130 135 140

Leu Asp Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln
145 150 155 160

Tyr Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro
165 170 175

Ser Val Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe
180 185 190

Lys Asn Ser Leu Thr Thr Leu Pro Met Gly Gly Lys Gly Gly Ser

195

200

205

Asp Phe Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys
210 215 220

Gln Ser Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp
225 230 235 240

Val Pro Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu
245 250 255

Phe Gly Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr
260 265 270

Pro Lys Gly Gln Glu Tyr Gly Ser Glu Ile Arg Pro Glu Ala Thr
275 280 285

Gly Tyr Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly
290 295 300

Glu Ser Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val
305 310 315 320

Ala Gln Tyr Cys Ala Glu Leu Leu Glu Lys Gly Ala Ile Val Leu
325 330 335

Ser Leu Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr
340 345 350

Arg Glu Gln Leu Gln Ala Val Gln Asp Met Lys Lys Asn Asn Ser
355 360 365

Ala Arg Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp
370 375 380

Arg Arg Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro
385 390 395 400

Cys Ala Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile

405

410

415

Lys His Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr
420 425 430

Asn Glu Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro
435 440 445

Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met
450 455 460

Thr Gln Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp
465 470 475 480

Lys Leu Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro
485 490 495

Ser Arg Arg Tyr Asn Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly
500 505 510

Phe Thr Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val
515 520 525

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 33..1568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10

UF-155CD3

CTCCTTCTG CTCGCCCTCT CTCCGTCCCG CC ATG CAG ACC GCC CTC GTC GCC
 Met Gln Thr Ala Leu Val Ala
 1 5

AAG CCT ATC GTG GCC TGC GCG TGG GTC CGC TCC GCC AAG CGC GAT GTC
 Lys Pro Ile Val Ala Cys Ala Trp Val Arg Ser Ala Lys Arg Asp Val
 10 15 20

CGC GCC AAG GCC GTC TCG CTG GAG GAG CAG ATC TCC GCG ATG GAC GCC
 Arg Ala Lys Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala
 25 30 35

ACC ACC GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG AAG CAG ATG GCC
 Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala
 40 45 50 55

ACC AAG GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC AAG AAC CCC GAC
 Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp
 60 65 70

GTG CGC CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC CCG GAG CAG CAG
 Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln
 75 80 85

GAG TTC ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC CTG CAG CCC GTG
 Glu Phe Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val
 90 95 100

TTC GAG AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG CAG ATC GTT GAG
 Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu
 105 110 115

CCT GAG CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG GAC GAC GCC GGC
 Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly
 120 125 130 135

AAC CTG CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC TCG TCC GCC ATC
 Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile
 140 145 150

GGC CCC TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC GTG AAC CTG TCC	533		
Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser			
155	160	165	
ATC ATG AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG AAC AGC CTG ACC	581		
Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr			
170	175	180	
ACC CTG CCC ATG GGC GGC AAG GGC GGC TCC GAC TTC GAC CCC AAG	629		
Thr Leu Pro Met Gly Gly Lys Gly Ser Asp Phe Asp Pro Lys			
185	190	195	
GGC AAG AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG TCC TTC ATG ACC	677		
Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr			
200	205	210	215
GAG CTG CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG CCC GCC GGC GAC	725		
Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp			
220	225	230	
ATC GGC GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC GGC CAG TAC AAG	773		
Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys			
235	240	245	
CGC ATC ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG AAG GGC CAG GAG	821		
Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu			
250	255	260	
TAT GGC GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC TAC GGC GCC GTG	869		
Tyr Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val			
265	270	275	
CTG TTT GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG AGC CTC AAG GGC	917		
Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly			
280	285	290	295
AAG CGC TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC CAG TAC TGC GCG	965		
Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala			
300	305	310	

12	UF-155CD3
GAG CTG CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG CTG TCC GAC TCC Glu Leu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser 315 320 325	1013
CAG GGC TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC GAG CAG CTG CAG Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln 330 335 340	1061
GCG GTG CAG GAC ATG AAG AAG AAC AAC AGC GCC CGC ATC TCC GAG Ala Val Gln Asp Met Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu 345 350 355	1109
TAC AAG AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC CGC AAG CCT TGG Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp 360 365 370 375	1157
GAG CTG GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC GCC ACC CAG AAC Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn 380 385 390	1205
GAG ATC GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG CAC GGC TGC CAG Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln 395 400 405	1253
TAC GTG GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC GAG GCC ATC CAC Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His 410 415 420	1301
AAG TAC AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC AAG GCG GCC AAC Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn 425 430 435	1349
GCC GGC GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC CAG AAC CGC ATG Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met 440 445 450 455	1397
AGC CTG AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG CTG GAG CGC ATC Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile 460 465 470	1445

13	UF-155CD3	
ATG AAG GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC CGC AGA TAC AAT	1493	
Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn		
475	480	485
GTT GAC CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC ACC AAG GTG GCT	1541	
Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala		
490	495	500
GAT GCC GTC AAG GCC CAG GGC GCT GTT TAAGCTGCC AGGCCAAGC	1588	
Asp Ala Val Lys Ala Gln Gly Ala Val		
505	510	
CACGGCTCAC CGGCAATCCA ACCCAACCAA CTCAACGGCC AGGACCTTTT CGGAAGCGGC	1648	
GCCTTTTCC CAGCCAGGGC CCTCACCTGC CCTTCATAA CCCTGCTATT GCCGCCGTGC	1708	
CCCTGCAATT CCACCCCAAG AAGAACTAGC GGCACTTGAC TGCATCAGGA CGGCTATTTT	1768	
TTTCGCGACG CGCGCTCACC CCGAGAGCCT CTCTCCCCG AGCCCTAACG GCTGACGTCC	1828	
GCCCGACTTT GCCTCGCACA TCGCTCGTT TTGACCCCCCT CCAGTCTACC CACCCCTGTTG	1888	
TGAAGCCTAC CAGCTCAATT GCCTTTAGT GTATGTGCGC CCCCTCCTGC CCCCCGAATTT	1948	
TCCTGCCATG AGACGTGCGG TTCCTAGCCT GGTGACCCCA AGTAGCAGTT AGTGTGCGTG	2008	
CCTTGCCCTG CGCTGCCCGG GATGCGATAC TGTGACCTGA GAGTGCTTGT GTAAACACGA	2068	
CGAGTCAAAA AAAAAAAA AAAAAAAA A	2099	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gln Thr Ala Leu Val Ala Lys Pro Ile Val Ala Cys Ala Trp Val
1 5 10 15

Arg Ser Ala Lys Arg Asp Val Arg Ala Lys Ala Val Ser Leu Glu Glu
20 25 30

Gln Ile Ser Ala Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln
35 40 45

Lys Ala Val Lys Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val
50 55 60

His Gly Ile Lys Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe
65 70 75 80

Met Lys Asp Pro Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val
85 90 95

Ala Val Ser Leu Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro
100 105 110

Ile Phe Lys Gln Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val
115 120 125

Ser Trp Leu Asp Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg
130 135 140

Val Gln Tyr Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe
145 150 155 160

His Pro Ser Val Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln
165 170 175

Ile Phe Lys Asn Ser Leu Thr Thr Leu Pro Met Gly Gly Lys Gly
180 185 190

Gly Ser Asp Phe Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg

195

200

205

Phe Cys Gln Ser Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val
210 215 220

Gln Asp Val Pro Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly
225 230 235 240

Tyr Leu Phe Gly Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val
245 250 255

Leu Thr Pro Lys Gly Gln Glu Tyr Gly Ser Glu Ile Arg Pro Glu
260 265 270

Ala Thr Gly Tyr Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp
275 280 285

Lys Gly Glu Ser Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly
290 295 300

Asn Val Ala Gln Tyr Cys Ala Glu Leu Leu Glu Lys Gly Ala Ile
305 310 315 320

Val Leu Ser Leu Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly
325 330 335

Phe Thr Arg Glu Gln Leu Gln Ala Val Gln Asp Met Lys Lys Asn
340 345 350

Asn Ser Ala Arg Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val
355 360 365

Gly Asp Arg Arg Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala
370 375 380

Phe Pro Cys Ala Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu
385 390 395 400

Leu Ile Lys His Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro

405

410

415

Ser Thr Asn Glu Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr
420 425 430

Cys Pro Gly Lys Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu
435 440 445

Glu Met Thr Gln Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val
450 455 460

Arg Asp Lys Leu Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met
465 470 475 480

Gly Pro Ser Arg Arg Tyr Asn Val Asp Leu Ala Ala Gly Ala Asn Ile
485 490 495

Ala Gly Phe Thr Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val
500 505 510

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr Thr Gly
1 5 10 15

Asp Phe Thr Ala
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CAGATCTCCG CGATGGACGC CACCACCGGC GACTTCACGG CGCTGCAGAA GGCGGTGAAG	60
CAGATGGCCA CCAAGGCCGG CACTGAGGGC CTGGTGCACG GCATCAAGAA CCCCCGACGTG	120
CGCCAGCTGC TGACCGAGAT CTTCATGAAG GACCCGGAGC AGCAGGAGTT CATGCAGGCG	180

GTGCGCGAGG TGGCCGTCTC CCTGCAGCCC GTGTCGAGA AGCGCCCCGA GCTGCTGCC	240
ATCTTCAAGC AGATCGTTGA GCCTGAGCGC GTGATCACCT TCCGCGTGTCTGGAC	300
GACGCCGGCA ACCTGCAGGT CAACCGCGGC TTCCCGGTGC AGTACTCGTC CGCCATCGGC	360
CCCTACAAGG GCGGCCTGCG CTTCCACCCC TCCGTGAACC TGTCCATCAT GAAGTTCC	420
GCCTTTGAGC AGATCTCAA GAACAGCCTG ACCACCCCTGC CCATGGGCGG CGGCAAGGGC	480
GGCTCCGACT TCGACCCCAA GGGCAAGAGC GACGCGGAGG TGATGCGCTT CTGCCAGTCC	540
TTCATGACCG AGCTGCAGCG CCACATCAGC TACGTGCAGG ACGTGCCCGC CGGGGACATC	600
GGCGTGGGCG CGCGCGAGAT TGGCTACCTT TTCGGCCAGT ACAAGCGCAT CACCAAGAAC	660
TACACCGGCG TGCTGACCCC GAAGGGCCAG GAGTATGGCG GCTCCGAGAT CCGCCCCGAG	720
GCCACCGGCT ACGGCGCCGT GCTGTTGTG GAGAACGTGC TGAAGGACAA GGGCGAGAGC	780
CTCAAGGGCA AGCGCTGCCT GGTGTCTGGC GCGGGCAACG TGGCCCAGTA CTGCGCGGAG	840
CTGCTGCTGG AGAAGGGCGC CATCGTGCTG TCGCTGTCCG ACTCCCAGGG CTACGTGTAC	900
GAGCCCAACG GCTTCACGCG CGAGCAGCTG CAGGGCGTGC AGGACATGAA GAAGAAGAAC	960
AACAGCGCCC GCATCTCCGA GTACAAGAGC GACACCGCCG TGTATGTGGG CGACCGCCGC	1020
AAGCCTTGGG AGCTGGACTG CCAGGTGGAC ATCGCCTTCC CCTGCGCCAC CCAGAACGAG	1080
ATCGATGAGC ACGACGCCGA GCTGCTGATC AAGCACGGCT GCCAGTACGT GGTGGAGGGC	1140
GCCAACATGC CCTCCACCAA CGAGGCCATC CACAAGTACA ACAAGGCCGG CATCATCTAC	1200
TGCCCGGGCA AGGCGGCCAA CGCCGGCGGC GTGGCGGTCA GCGGCCTGGA GATGACCCAG	1260
AACCGCATGA GCCTGAACTG GACTCGCGAG GAGGTTCGCG ACAAGCTGGA GCGCATCATG	1320
AAGGACATCT ACGACTCCGC CATGGGGCCG TCCCGCAGAT ACAATGTTGA CCTGGCTGCG	1380

19	UF-155CD3
GGCGCCAACA TCGCGGGCTT CACCAAGGTG GCTGATGCCG TCAAGGCCA GGGCGCTGTT	1440
TAAGCTGCCA AGGCCAAGC CACGGCTCAC CGGCAATCCA ACCCAACCAA CTCAACGGCC	1500
AGGACCTTTT CGGAAGCGGC GCCTTTTCC CAGCCAGGGC CCTCACCTGC CCTTTCATAA	1560
CCCTGCTATT GCCGCCGTGC CCCTGCAATT CCACCCCAAG AAGAACTAGC GGCACTTGAC	1620
TGCATCAGGA CGGCTATTTT TTTCGCGACG CGCGCTCACC CCGAGAGCCT CTCTCCCCG	1680
AGCCCTAACG GCTGACGTCC GCCCGACTTT GCCTCGCACA TCGCTCGGTT TTGACCCCT	1740
CCAGTCTACC CACCCCTGTTG TGAAGCCTAC CAGCTCAATT GCCTTTAGT GTATGTGCGC	1800
CCCCTCCTGC CCCCGAATTTC TCCTGCCATG AGACGTGCGG TTCCTAGCCT GGTGACCCCA	1860
AGTAGCAGTT AGTGTGCGTG CCTTGCCCTG CGCTGCCCGG GATGCGATAAC TGTGACCTGA	1920
GAGTGCTTGT GTAAACACGA CGAGTCAAAA AAAAAAAA AAAAAAAA	1969

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CTCAAAGGCA AGGAACCTCA TG	22
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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCGACAT TCTAGACAGA ATTCGTGGAT CCTTTTTTTT TTTTTTTTT

50

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGACGAGTAC TGCACGC

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GATCTCGGTC AGCAGCTG

18

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GGGTCGACAT TCTAGACAGA A

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGGTCGACAT TCTAGACAGA ATTCTGGAT CCTTTTTTTT TTTTTTTTTT TTTTTCTCC 60

TTTCTGCTCG CCCTCTCTCC GTCCCGCCAT GCAGACCGCC CTCGTCGCCA AGCCTATCGT 120

GGCCGCCCG CTGGCGGCAC GCCCGCGCTG CCTCGCGCCG TGGCCGTGCG CGTGGGTCCG 180

CTCCGCCAAG CGCGATGTCC GCGCCAAGGC CGTCTCGCTG GAGGAGCAGA TCTCCGCGAT 240

GGACGCCACC ACCGGCGACT TCACGGCGCT GCAGAAGGCG GTGAAGCAGA TGGCCACCAA 300

GGCGGGCACT GAGGGCCTGG TGCACGGCAT CAAGAACCCC GACGTGCGCC AGCTGCTGAC 360

CGAGATC

367

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGGTCGACAT TCTAGACAGA ATTCGTGGAT CCTTTTTTT TTTTTTTTT TTTTTCTCC	60
TTTCTGCTCG CCCTCTCTCC GTCCCGCCAT GCAGACCGCC CTCGTCGCCA AGCCTATCGT	120
GGCCTGCGCG TGGGTCCGCT CCGCCAAGCG CGATGTCCGC GCCAAGGCCG TCTCGCTGGA	180
GGAGCAGATC TCCGCGATGG ACGCCACCAC CGGCGACTTC ACGGCGCTGC AGAAGGCGGT	240
GAAGCAGATG GCCACCAAGG CGGGCACTGA GGGCCTGGTG CACGGCATCA AGAACCCGA	300
CGTGCGCCAG CTGCTGACCG AGATC	325

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTTTCTGCTC GCCCTCTC

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTTTCTGCTC GCCCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCGCCCG GCTGGCGGCA CGCCCGCGCT GCCTCGCGCC GTGGCCGTGC GCGTGGGTCC.	120
GCTCCGCCAA GCGCGATGTC CGCGCCAAGG CCGTCTCGCT GGAGGAGCAG ATCTCCGCGA	180
TGGACGCCAC CACCGGCGAC TTCACGGCGC TGCAGAAGGC GGTGAAGCAG ATGGCCACCA	240
AGGCAGGGCAC TGAGGGCCTG GTGCACGGCA TCAAGAACCC CGACGTGCGC CAGCTGCTGA	300
CCGAGATC	308

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCTGCGC GTGGGTCCGC TCCGCCAAGC GCGATGTCCG CGCCAAGGCC GTCTCGCTGG	120
AGGAGCAGAT CTCCGCGATG GACGCCACCA CCGGCGACTT CACGGCGCTG CAGAAGGC GG	180
TGAAGCAGAT GGCCACCAAG GCGGGCACTG AGGGCCTGGT GCACGGCATC AAGAACCCCG	240
ACGTGCGCCA GCTGCTGACC GAGATC	266

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCGCCCG CGTGGCGGCA CGCCCGCGCT GCCTCGCGCC GTGGCCGTGC GCGTGGGTCC	120
GCTCCGCCAA GCGCGATGTC CGCGCCAAGG CCGTCTCGCT GGAGGAGCAG ATCTCCGCGA	180
TGGACGCCAC CACCGGCGAC TTCACGGCGC TGCAGAAGGC GGTGAAGCAG ATGGCCACCA	240
AGGCGGGCAC TGAGGGCCTG GTGCACGGCA TCAAGAACCC CGACGTGCGC CAGCTGCTGA	300
CCGAGATCTT CATGAAGGAC CCGGAGCAGC AGGAGTTCAT GCAGGGGGTG CGCGAGGTGG	360
CCGTCTCCCT GCAGCCCGTG TTCGAGAACG GCCCCGAGCT GCTGCCATC TTCAAGCAGA	420
TCGTTGAGCC TGAGCGCGTG ATCACCTTCC GCGTGTCCCTG GCTGGACGAC GCCGGCAACC	480

25	UF-155CD3
TGCAGGTCAA CCGCGGCTTC CGCGTGCAGT ACTCGTCCGC CATCGGCCCG TACAAGGGCG	540
GCCTGCGCTT CCACCCCTCC GTGAACCTGT CCATCATGAA GTTCCTTGCC TTTGAGCAGA	600
TCTTCAAGAA CAGCCTGACC ACCCTGCCA TGGGCGGCAG CAAGGGCGGC TCCGACTTCG	660
ACCCCAAGGG CAAGAGCGAC GCGGAGGTGA TGCGCTTCTG CCAGTCCTTC ATGACCGAGC	720
TGCAGCGCCA CATCAGCTAC GTGCAGGACG TGCCCGCCGG CGACATCGGC GTGGGCGCGC	780
GCGAGATTGG CTACCTTTTC GGCCAGTACA AGCGCATCAC CAAGAACTAC ACCGGCGTGC	840
TGACCCCGAA GGGCCAGGAG TATGGCGGCT CCGAGATCCG CCCCAGGGCC ACCGGCTACG	900
GCGCCGTGCT GTTTGTGGAG AACGTGCTGA AGGACAAGGG CGAGAGCCTC AAGGGCAAGC	960
GCTGCCTGGT GTCTGGCGCG GGCAACGTGG CCCAGTACTG CGCGGAGCTG CTGCTGGAGA	1020
AGGGCGCCAT CGTGCTGTCG CTGTCCGACT CCCAGGGCTA CGTGTACGAG CCCAACGGCT	1080
TCACGCGCGA GCAGCTGCAG GCGGTGCAGG ACATGAAGAA GAAGAACAAAC AGCGCCCGCA	1140
TCTCCGAGTA CAAGAGCGAC ACCGCCGTGT ATGTGGCGA CCGCCGCAAG CCTTGGGAGC	1200
TGGACTGCCA GGTGGACATC GCCTTCCCT GCGCCACCCA GAACGAGATC GATGAGCACG	1260
ACGCCGAGCT GCTGATCAAG CACGGCTGCC AGTACGTGGT GGAGGGCGCC AACATGCCCT	1320
CCACCAACGA GGCCATCCAC AAGTACAACA AGGCCGGCAT CATCTACTGC CCCGGCAAGG	1380
CGGCCAACGC CGGCGGCGTG GCGGTCAAGCG GCCTGGAGAT GACCCAGAAC CGCATGAGCC	1440
TGAACCTGGAC TCGCGAGGAG GTTCGCGACA AGCTGGAGCG CATCATGAAG GACATCTACG	1500
ACTCCGCCAT GGGGCCGTCC CGCAGATACA ATGTTGACCT GGCTGCGGGC GCCAACATCG	1560
CGGGCTTCAC CAAGGTGGCT GATGCCGTCA AGGCCAGGG CGCTGTTAA GCTGCCAGG	1620
CCCAAGCCAC GGCTCACCGG CAATCCAACC CAACCAACTC AACGGCCAGG ACCTTTCGG	1680

AAGCGGCGCC TTTTCCCAG CCAGGGCCCT CACCTGCCCT TTCATAACCC TGCTATTGCC	1740
GCCGTGCCCT TGCAATTCCA CCCCAAGAAG AACTAGCGC ACTTGACTGC ATCAGGACGG	1800
CTATTTTTTG CGCGACGCGC GCTCACCCCG AGAGCCTCTC TCCCCCGAGC CCTAAGCGCT	1860
GACGTCCGCC CGACTTTGCC TCGCACATCG CTCGGTTTG ACCCCCTCCA GTCTACCCAC	1920
CCTGTTGTGA AGCCTACCAAG CTCAATTGCC TTTTAGTGTG TGTGCGCCCC CTCCTGCCCT	1980
CGAATTTCC TGCCATGAGA CGTGCAGGTTCTAGCCTGGT GACCCCAAGT AGCAGTTAGT	2040
GTCGTGCCT TGCCCTGCGC TGCCCGGGAT GCGATACTGT GACCTGAGAG TGCTTGTGTA	2100
AACACGACGA GTCAAAAAAA AAAAAAAA AAAAAAA	2137

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2096 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTTTCTGCTC GCCCTCTCTC CGTCCCGCCA TGCAGACCGC CCTCGTCGCC AAGCCTATCG	60
TGGCCTGCGC GTGGGTCCGC TCCGCCAAGC GCGATGTCCG CGCCAAGGCC GTCTCGCTGG	120
AGGAGCAGAT CTCCCGATG GACGCCACCA CCGGCGACTT CACGGCGCTG CAGAAGGCGG	180
TGAAGCAGAT GGCCACCAAG GCGGGCACTG AGGGCCTGGT GCACGGCATC AAGAACCCCG	240
ACGTGCGCCA GCTGCTGACC GAGATCTTCA TGAAGGACCC GGAGCAGCAG GAGTCATGC	300

AGGCGGTGCG CGAGGTGGCC GTCTCCCTGC AGCCCGTGT CGAGAAGCGC CCCGAGCTGC	360
TGCCCATCTT CAAGCAGATC GTTGAGCCTG AGCGCGTGAT CACCTTCCGC GTGTCCCTGGC	420
TGGACGACGC CGGCAACCTG CAGGTCAACC GCGGCTTCCG CGTGCAGTAC TCGTCCGCCA	480
TCGGCCCCTA CAAGGGCGGC CTGCGCTTCC ACCCCTCCGT GAACCTGTCC ATCATGAAGT	540
TCCTTGCCTT TGAGCAGATC TTCAAGAACAA GCCTGACCAC CCTGCCCATG GGCGGCGGCA	600
AGGGCGGCTC CGACTTCGAC CCCAAGGGCA AGAGCGACGC GGAGGTGATG CGCTTCTGCC	660
AGTCCTTCAT GACCGAGCTG CAGCGCCACA TCAGCTACGT GCAGGACGTG CCCGCCGGCG	720
ACATCGGCGT GGGCGCGCGC GAGATTGGCT ACCTTTCGG CCAGTACAAG CGCATCACCA	780
AGAACTACAC CGGCGTGCTG ACCCGAAGG GCCAGGAGTA TGGCGGCTCC GAGATCCGCC	840
CCGAGGCCAC CGGCTACGGC GCCGTGCTGT TTGTGGAGAA CGTGTGAAG GACAAGGGCG	900
AGAGCCTCAA GGGCAAGCGC TGCCTGGTGT CTGGCGCGGG CAACGTGGCC CAGTACTGCG	960
CGGAGCTGCT GCTGGAGAAG GGCGCCATCG TGCTGTCGCT GTCCGACTCC CAGGGCTACG	1020
TGTACGAGCC CAACGGCTTC ACGCGCGAGC AGCTGCAGGC GGTGCAGGAC ATGAAGAAGA	1080
AGAACAAACAG CGCCCGCATC TCCGAGTACA AGAGCGACAC CGCCGTGTAT GTGGGCGACC	1140
GCCGCAAGCC TTGGGAGCTG GACTGCCAGG TGGACATCGC CTTCCCCCTGC GCCACCCAGA	1200
ACGAGATCGA TGAGCACGAC GCCGAGCTGC TGATCAAGCA CGGCTGCCAG TACGTGGTGG	1260
AGGGCGCCAA CATGCCCTCC ACCAACGAGG CCATCCACAA GTACAACAAG GCCGGCATCA	1320
TCTACTGCC CGGCAAGGCG GCCAACGCCG GCGGCGTGGC GGTCAAGCGGC CTGGAGATGA	1380
CCCAGAACCG CATGAGCCTG AACTGGACTC GCGAGGGAGGT TCGCGACAAG CTGGAGCGCA	1440
TCATGAAGGA CATCTACGAC TCCGCCATGG GGCGTCCCG CAGATACAAT GTTGACCTGG	1500

CTGCGGGCGC	CAACATCGCG	GGCTTCACCA	AGGTGGCTGA	TGCCGTCAAG	GCCCAGGGCG	1560
CTGTTTAAGC	TGCCAGGCC	CAAGCCACGG	CTCACCGGCA	ATCCAACCCA	ACCAACTCAA	1620
CGGCCAGGAC	CTTTCGGAA	GCGGCGCCTT	TTTCCCAGCC	AGGGCCCTCA	CCTGCCCTTT	1680
CATAACCCCTG	CTATTGCCGC	CGTCCCCCTG	CAATTCCACC	CCAAGAAGAA	CTAGCGGCAC	1740
TTGACTGCAT	CAGGACGGCT	ATTTTTTCG	CGACGCGCGC	TCACCCCGAG	AGCCTCTCTC	1800
CCCCGAGCCC	TAAGCGCTGA	CGTCCGCCCG	ACTTGCCTC	GCACATCGCT	CGGTTTGAC	1860
CCCCCTCCAGT	CTACCCACCC	TGTTGTGAAG	CCTACCAGCT	CAATTGCCCTT	TTAGTGTATG	1920
TGCGCCCCCT	CCTGCCCG	AATTTCCCTG	CCATGAGACG	TGCGGTTCCCT	AGCCTGGTGA	1980
CCCCAAGTAG	CAGTTAGTGT	GCGTGCCTTG	CCCTGCGCTG	CCCGGGATGC	GATACTGTGA	2040
CCTGAGAGTG	CTTGTGTAAA	CACGACGAGT	AAAAAAAAAA	AAAAAAAAAA	AAAAAA	2096

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATATGGCCG	TCTCGCTGGG	AGGAG	25
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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGGATTGC CGGTGAGCC

19

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATATGGACCG CCACCACCGG C

21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 4..1464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAT ATG GCC GTC TCG CTG GAG GAG CAG ATC TCC GCG ATG GAC GCC ACC	48		
Met Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr			
515	520	525	
ACC GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG AAG CAG ATG GCC ACC	96		
Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala Thr			
530	535	540	
AAG GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC AAG AAC CCC GAC GTG	144		
Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp Val			
545	550	555	
CGC CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC CCG GAG CAG CAG GAG	192		
Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln Glu			
560	565	570	575
TTC ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC CTG CAG CCC GTG TTC	240		
Phe Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val Phe			
580	585	590	
GAG AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG CAG ATC GTT GAG CCT	288		
Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu Pro			
595	600	605	
GAG CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG GAC GAC GCC GGC AAC	336		
Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly Asn			
610	615	620	
CTG CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC TCG TCC GCC ATC GGC	384		
Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile Gly			
625	630	635	
CCC TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC GTG AAC CTG TCC ATC	432		
Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile			
640	645	650	655

ATG AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG AAC AGC CTG ACC ACC	480		
Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr Thr			
660	665	670	
CTG CCC ATG GGC GGC AAG GGC GGC TCC GAC TTC GAC CCC AAG GGC	528		
Leu Pro Met Gly Gly Lys Gly Ser Asp Phe Asp Pro Lys Gly			
675	680	685	
AAG AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG TCC TTC ATG ACC GAG	576		
Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr Glu			
690	695	700	
CTG CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG CCC GCC GGC GAC ATC	624		
Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp Ile			
705	710	715	
GGC GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC GGC CAG TAC AAG CGC	672		
Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys Arg			
720	725	730	735
ATC ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG AAG GGC CAG GAG TAT	720		
Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu Tyr			
740	745	750	
GGC GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC TAC GGC GCC GTG CTG	768		
Gly Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val Leu			
755	760	765	
TTT GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG AGC CTC AAG GGC AAG	816		
Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly Lys			
770	775	780	
CGC TGC CTG GTG TCT GGC GCG AAC GTG GCC CAG TAC TGC GCG GAG	864		
Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala Glu			
785	790	795	
CTG CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG CTG TCC GAC TCC CAG	912		
Leu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser Gln			
800	805	810	815

GGC TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC GAG CAG CTG CAG GCG			960
Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln Ala			
820	825	830	
GTG CAG GAC ATG AAG AAG AAC AAC AGC GCC CGC ATC TCC GAG TAC			1008
Val Gln Asp Met Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu Tyr			
835	840	845	
AAG AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC CGC AAG CCT TGG GAG			1056
Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp Glu			
850	855	860	
CTG GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC GCC ACC CAG AAC GAG			1104
Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn Glu			
865	870	875	
ATC GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG CAC GGC TGC CAG TAC			1152
Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln Tyr			
880	885	890	895
GTG GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC GAG GCC ATC CAC AAG			1200
Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His Lys			
900	905	910	
TAC AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC AAG GCG GCC AAC GCC			1248
Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn Ala			
915	920	925	
GGC GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC CAG AAC CGC ATG AGC			1296
Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met Ser			
930	935	940	
CTG AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG CTG GAG CGC ATC ATG			1344
Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile Met			
945	950	955	
AAG GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC CGC AGA TAC AAT GTT			1392
Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn Val			
960	965	970	975

33	UF-155CD3	
GAC CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC ACC AAG GTG GCT GAT	1440	
Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala Asp		
980	985	990
GCC GTC AAG GCC CAG GGC GCT GTT TAAGCTGCC AGGCCAAGC CACGGCTCAC	1494	
Ala Val Lys Ala Gln Gly Ala Val		
995		
CGGCAATCCA AC	1506	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ala Val Ser Leu Glu Glu Gln Ile Ser Ala Met Asp Ala Thr Thr
 1 5 10 15

Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys Gln Met Ala Thr Lys
 20 25 30

Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys Asn Pro Asp Val Arg
 35 40 45

Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro Glu Gln Gln Glu Phe
 50 55 60

Met Gln Ala Val Arg Glu Val Ala Val Ser Leu Gln Pro Val Phe Glu
 65 70 75 80

Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln Ile Val Glu Pro Glu
 85 90 95

Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp Asp Ala Gly Asn Leu
100 105 110

Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser Ser Ala Ile Gly Pro
115 120 125

Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val Asn Leu Ser Ile Met
130 135 140

Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn Ser Leu Thr Thr Leu
145 150 155 160

Pro Met Gly Gly Lys Gly Gly Ser Asp Phe Asp Pro Lys Gly Lys
165 170 175

Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser Phe Met Thr Glu Leu
180 185 190

Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro Ala Gly Asp Ile Gly
195 200 205

Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly Gln Tyr Lys Arg Ile
210 215 220

Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys Gly Gln Glu Tyr Gly
225 230 235 240

Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr Gly Ala Val Leu Phe
245 250 255

Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser Leu Lys Gly Lys Arg
260 265 270

Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln Tyr Cys Ala Glu Leu
275 280 285

Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu Ser Asp Ser Gln Gly
290 295 300

Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu Gln Leu Gln Ala Val
305 310 315 320

Gln Asp Met Lys Lys Asn Asn Ser Ala Arg Ile Ser Glu Tyr Lys
325 330 335

Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg Lys Pro Trp Glu Leu
340 345 350

Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala Thr Gln Asn Glu Ile
355 360 365

Asp Glu His Asp Ala Glu Leu Leu Ile Lys His Gly Cys Gln Tyr Val
370 375 380

Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu Ala Ile His Lys Tyr
385 390 395 400

Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys Ala Ala Asn Ala Gly
405 410 415

Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln Asn Arg Met Ser Leu
420 425 430

Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu Glu Arg Ile Met Lys
435 440 445

Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg Arg Tyr Asn Val Asp
450 455 460

Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr Lys Val Ala Asp Ala
465 470 475 480

Val Lys Ala Gln Gly Ala Val
485

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: CDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1431

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAT ATG GAC GCC ACC ACC GGC GAC TTC ACG GCG CTG CAG AAG GCG GTG	48	
Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val		
490	495	500
AAG CAG ATG GCC ACC AAG GCG GGC ACT GAG GGC CTG GTG CAC GGC ATC	96	
Lys Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile		
505	510	515
AAG AAC CCC GAC GTG CGC CAG CTG CTG ACC GAG ATC TTC ATG AAG GAC	144	
Lys Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp		
520	525	530
CCG GAG CAG CAG GAG TTC ATG CAG GCG GTG CGC GAG GTG GCC GTC TCC	192	
Pro Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val Ala Val Ser		
535	540	545
550		
CTG CAG CCC GTG TTC GAG AAG CGC CCC GAG CTG CTG CCC ATC TTC AAG	240	
Leu Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys		
555	560	565
CAG ATC GTT GAG CCT GAG CGC GTG ATC ACC TTC CGC GTG TCC TGG CTG	288	
Gln Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu		
570	575	580
GAC GAC GCC GGC AAC CTG CAG GTC AAC CGC GGC TTC CGC GTG CAG TAC	336	

Asp Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr			
585	590	595	
TCG TCC GCC ATC GGC CCC TAC AAG GGC GGC CTG CGC TTC CAC CCC TCC			384
Ser Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser			
600	605	610	
GTG AAC CTG TCC ATC ATG AAG TTC CTT GCC TTT GAG CAG ATC TTC AAG			432
Val Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys			
615	620	625	630
AAC AGC CTG ACC ACC CTG CCC ATG GGC GGC GGC AAG GGC GGC TCC GAC			480
Asn Ser Leu Thr Thr Leu Pro Met Gly Gly Lys Gly Ser Asp			
635	640	645	
TTC GAC CCC AAG GGC AAG AGC GAC GCG GAG GTG ATG CGC TTC TGC CAG			528
Phe Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln			
650	655	660	
TCC TTC ATG ACC GAG CTG CAG CGC CAC ATC AGC TAC GTG CAG GAC GTG			576
Ser Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val			
665	670	675	
CCC GCC GGC GAC ATC GGC GTG GGC GCG CGC GAG ATT GGC TAC CTT TTC			624
Pro Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe			
680	685	690	
GGC CAG TAC AAG CGC ATC ACC AAG AAC TAC ACC GGC GTG CTG ACC CCG			672
Gly Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro			
695	700	705	710
AAG GGC CAG GAG TAT GGC GGC TCC GAG ATC CGC CCC GAG GCC ACC GGC			720
Lys Gly Gln Glu Tyr Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly			
715	720	725	
TAC GGC GCC GTG CTG TTT GTG GAG AAC GTG CTG AAG GAC AAG GGC GAG			768
Tyr Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu			
730	735	740	

AGC CTC AAG GGC AAG CGC TGC CTG GTG TCT GGC GCG GGC AAC GTG GCC	816		
Ser Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala			
745	750	755	
CAG TAC TGC GCG GAG CTG CTG GAG AAG GGC GCC ATC GTG CTG TCG	864		
Gln Tyr Cys Ala Glu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser			
760	765	770	
CTG TCC GAC TCC CAG GGC TAC GTG TAC GAG CCC AAC GGC TTC ACG CGC	912		
Leu Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg			
775	780	785	790
GAG CAG CTG CAG GCG GTG CAG GAC ATG AAG AAG AAC AAC AGC GCC	960		
Glu Gln Leu Gln Ala Val Gln Asp Met Lys Lys Lys Asn Asn Ser Ala			
795	800	805	
CGC ATC TCC GAG TAC AAG AGC GAC ACC GCC GTG TAT GTG GGC GAC CGC	1008		
Arg Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg			
810	815	820	
CGC AAG CCT TGG GAG CTG GAC TGC CAG GTG GAC ATC GCC TTC CCC TGC	1056		
Arg Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys			
825	830	835	
GCC ACC CAG AAC GAG ATC GAT GAG CAC GAC GCC GAG CTG CTG ATC AAG	1104		
Ala Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys			
840	845	850	
CAC GGC TGC CAG TAC GTG GTG GAG GGC GCC AAC ATG CCC TCC ACC AAC	1152		
His Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn			
855	860	865	870
GAG GCC ATC CAC AAG TAC AAC AAG GCC GGC ATC ATC TAC TGC CCC GGC	1200		
Glu Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly			
875	880	885	
AAG GCG GCC AAC GCC GGC GTG GCG GTC AGC GGC CTG GAG ATG ACC	1248		
Lys Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr			
890	895	900	

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CAG AAC CGC ATG AGC CTG AAC TGG ACT CGC GAG GAG GTT CGC GAC AAG	1296		
Gln Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys			
905	910	915	
CTG GAG CGC ATC ATG AAG GAC ATC TAC GAC TCC GCC ATG GGG CCG TCC	1344		
Leu Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser			
920	925	930	
CGC AGA TAC AAT GTT GAC CTG GCT GCG GGC GCC AAC ATC GCG GGC TTC	1392		
Arg Arg Tyr Asn Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe			
935	940	945	950
ACC AAG GTG GCT GAT GCC GTC AAG GCC CAG GGC GCT GTT TAAGCTGCC	1441		
Thr Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val			
955	960		
AGGCCCAAGC CACGGCTCAC CGGCAATCCA AC	1473		

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Asp Ala Thr Thr Gly Asp Phe Thr Ala Leu Gln Lys Ala Val Lys			
1	5	10	15
Gln Met Ala Thr Lys Ala Gly Thr Glu Gly Leu Val His Gly Ile Lys			
20	25	30	
Asn Pro Asp Val Arg Gln Leu Leu Thr Glu Ile Phe Met Lys Asp Pro			
35	40	45	

Glu Gln Gln Glu Phe Met Gln Ala Val Arg Glu Val Ala Val Ser Leu
50 55 60

Gln Pro Val Phe Glu Lys Arg Pro Glu Leu Leu Pro Ile Phe Lys Gln
65 70 75 80

Ile Val Glu Pro Glu Arg Val Ile Thr Phe Arg Val Ser Trp Leu Asp
85 90 95

Asp Ala Gly Asn Leu Gln Val Asn Arg Gly Phe Arg Val Gln Tyr Ser
100 105 110

Ser Ala Ile Gly Pro Tyr Lys Gly Gly Leu Arg Phe His Pro Ser Val
115 120 125

Asn Leu Ser Ile Met Lys Phe Leu Ala Phe Glu Gln Ile Phe Lys Asn
130 135 140

Ser Leu Thr Thr Leu Pro Met Gly Gly Lys Gly Ser Asp Phe
145 150 155 160

Asp Pro Lys Gly Lys Ser Asp Ala Glu Val Met Arg Phe Cys Gln Ser
165 170 175

Phe Met Thr Glu Leu Gln Arg His Ile Ser Tyr Val Gln Asp Val Pro
180 185 190

Ala Gly Asp Ile Gly Val Gly Ala Arg Glu Ile Gly Tyr Leu Phe Gly
195 200 205

Gln Tyr Lys Arg Ile Thr Lys Asn Tyr Thr Gly Val Leu Thr Pro Lys
210 215 220

Gly Gln Glu Tyr Gly Ser Glu Ile Arg Pro Glu Ala Thr Gly Tyr
225 230 235 240

Gly Ala Val Leu Phe Val Glu Asn Val Leu Lys Asp Lys Gly Glu Ser
245 250 255

Leu Lys Gly Lys Arg Cys Leu Val Ser Gly Ala Gly Asn Val Ala Gln
260 265 270

Tyr Cys Ala Glu Leu Leu Glu Lys Gly Ala Ile Val Leu Ser Leu
275 280 285

Ser Asp Ser Gln Gly Tyr Val Tyr Glu Pro Asn Gly Phe Thr Arg Glu
290 295 300

Gln Leu Gln Ala Val Gln Asp Met Lys Lys Asn Asn Ser Ala Arg
305 310 315 320

Ile Ser Glu Tyr Lys Ser Asp Thr Ala Val Tyr Val Gly Asp Arg Arg
325 330 335

Lys Pro Trp Glu Leu Asp Cys Gln Val Asp Ile Ala Phe Pro Cys Ala
340 345 350

Thr Gln Asn Glu Ile Asp Glu His Asp Ala Glu Leu Leu Ile Lys His
355 360 365

Gly Cys Gln Tyr Val Val Glu Gly Ala Asn Met Pro Ser Thr Asn Glu
370 375 380

Ala Ile His Lys Tyr Asn Lys Ala Gly Ile Ile Tyr Cys Pro Gly Lys
385 390 395 400

Ala Ala Asn Ala Gly Gly Val Ala Val Ser Gly Leu Glu Met Thr Gln
405 410 415

Asn Arg Met Ser Leu Asn Trp Thr Arg Glu Glu Val Arg Asp Lys Leu
420 425 430

Glu Arg Ile Met Lys Asp Ile Tyr Asp Ser Ala Met Gly Pro Ser Arg
435 440 445

Arg Tyr Asn Val Asp Leu Ala Ala Gly Ala Asn Ile Ala Gly Phe Thr
450 455 460

Lys Val Ala Asp Ala Val Lys Ala Gln Gly Ala Val

465

470

475